

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Li et al.

Application No: 09/348,815

Filed: July 8, 1999

For: **Connective Tissue Growth Factor-2**



Art Unit: 1635

Examiner: Zara, J.

Attorney Docket No: PF126P1D1

1635
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OCT 25 2000

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#8/declara

Declaration Of Donna Dimke Under 37 C.F.R. § 1.132

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

I, Donna Dimke, hereby declare and state as follows:

1. I am employed by Human Genome Sciences, Inc. (HGS), Rockville, Maryland, as Group Leader of Gene Discovery. Since I began working at HGS in March of 1993, my duties have primarily included carrying out and analyzing, as both a bench scientist and a manager, extensive DNA sequencing.

2. A partially redacted copy of the American Type Culture Collection (ATCC) deposit receipt for deposit number 75804 is attached hereto as Exhibit A. As the deposit receipt indicates, ATCC deposit number 75804 contains a DNA plasmid assigned the HGS Code Number 242,847, also known within HGS as HGS Clone ID HLFBE49XX. Exhibit B is a partially redacted Sequence Worksheet printout from the HGS electronic notebook for HGS Code Number 242,847, which shows the nucleotide sequence of HGS Code Number 242,847 and the correlation between this code number and HGS Clone ID HLFBE49XX. I requested from the ATCC a sample of ATCC deposit 75804 by a purchase order numbered 70038 dated May 15, 2000 (a partially redacted copy of which is attached hereto as Exhibit C). I received the sample of ATCC deposit 75804 from the ATCC in June of 2000, as

evidenced by Sales Order # SO171485 from the ATCC (a partially redacted copy of which is attached hereto as Exhibit D).

3. I determined the nucleotide sequence of the cDNA clone contained in the sample of the ATCC deposit number 75804 that I received from the ATCC in June of 2000. I have been shown what has been presented to me as Figures 1A-C as originally filed in U.S. Application No. 08/459,101 (hereinafter "original Figures 1A-C"), a copy of which original Figures 1A-C is attached hereto as Exhibit E. I used the nucleotide sequence of HGS Code 242,847, the coding portion of which is shown in original Figures 1A-C, as a reference to determine the nucleotide sequence of the cDNA clone contained in the plasmid of ATCC deposit number 75804. A sample of ATCC deposit number 75804 was thoroughly sequenced under my supervision in my laboratory at HGS. More specifically, a single plasmid isolate obtained from the sample of ATCC deposit number 75804 was initially identified by obtaining sequence information from near the 5'-end of the clone. Then, 20-mer primers were designed based on the HGS Code 242,847 nucleotide sequence to obtain sequence information covering the clone two to nine times over. The sequencing was carried out on an Applied Biosystems, Inc. (ABI) 377 automated sequencer using the ABI dye terminator kit, according to the manufacturer's instructions. The data obtained from this sequence analysis is summarized in Exhibit F, attached hereto, which shows an alignment of the individual sequencing runs performed on the sample of ATCC deposit number 75804 I received, as well as the sequence originally assigned to Clone ID HLFBE49XX (*i.e.*, HGS Code 242,847).

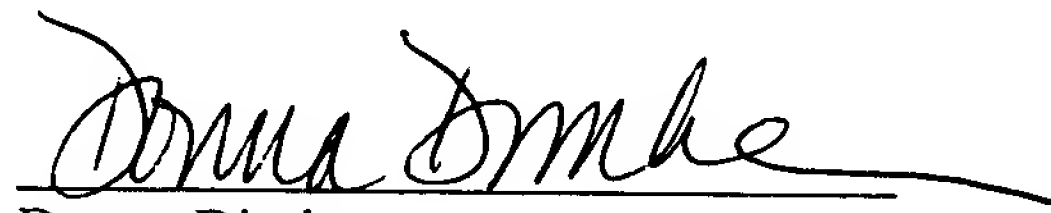
4. The correct nucleotide and encoded amino acid sequence for the cDNA clone contained in ATCC Deposit Number 75804 is shown in the corrected version of Figures 1A-C attached hereto as Exhibit G. Exhibit H is a marked up version of original Figures 1A-C showing in red ink the differences between the nucleotide and amino acid sequence in the

original figures and the correct nucleotide and encoded amino acid sequence of the cDNA clone of ATCC Deposit Number 75804 of Exhibit G.

5. Based on the experiments described above and the high degree of similarity between the nucleotide and amino acid sequences of original Figures 1A-C and the correct corresponding sequences as shown in Exhibit H, it is my belief that a person of ordinary skill in the art, upon routine sequencing of the cDNA of clone contained in ATCC deposit number 75804 using methods well known in the art prior to July 12, 1994, would readily determine that the correct sequence of the cDNA clone is the sequence shown in Exhibit G, especially when using original Figures 1A-C as a guide.

6. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application captioned above or any patent issuing thereupon.

Date: 10/17/00


Donna Dimke



American Type Culture Collection

12301 Parklawn Drive • Rockville, MD 20852 USA • Telephone: (301)231-5520 Telex: 898-055 ATCCNORTH • FAX: 301-770-2587

PF 126

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3 AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

To: (Name and Address of Depositor or Attorney)

Human Genome Sciences, Inc.
Attention: Craig A. Rosen, Ph.D.
9620 Medical Center Drive, Suite 300
Rockville, MD 20850

Deposited on Behalf of: Human Genome Sciences, Inc.

Identification Reference by Depositor:

ATCC Designation

DNA Plasmid, 242,847

75804

The deposits were accompanied by: ☐ a scientific description ☐ a proposed taxonomic description indicated above.

The deposits were received June 7, 1994 by this International Depository Authority and have been accepted.

AT YOUR REQUEST:

☒ We will inform you of requests for the strains for 30 years.

The strains will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strains.

If the cultures should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace them with living cultures of the same.

The strains will be maintained for a period of at least 30 years after the date of deposit, and for a period of at least five years after the most recent request for a sample. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the cultures cited above was tested June 14, 1994. On that date, the cultures were viable.

International Depository Authority: American Type Culture Collection, Rockville, Md. 20852 USA

Signature of person having authority to represent ATCC:

Bobbie A. Brandon
Bobbie A. Brandon, Head, ATCC Patent Depository

Date: June 20, 1994

cc: Greg Ferraro

REDACTED

Sequence Information

Gene Name: Homo sapiens mRNA for hCYR61 protein.

HGS Code: 242847

Sequence ID: HLFBE49XX

Search Results

Sequence

>HLFBE49XX
GGCAGGAGCC CGCCCGGGCC AGCCCTGGCC TCCCTGCCCA CCGGCCCAAC GCGCCGCACC
CCGACCCCGC TCGGAGCGGC TGTCGGCTGC ACAACAGCTT GTTGGTGTCT TGTGGGGCC
GCTGGCCCGG GGTACTCTCT GCGGACACA ATGAGCTGCC GAATGTTCAG GGAGCTGGCC
TTAGTGTCTA CCTTCTCCA CTTGACCAGG GTGGGGCTCT CCACCTGCC CCTTGACTTC
CACTGCCCCC TGGAGGGGCC CAAGTCGGC CAAGCAGCTC AACGAGGACT GCAGAAAAC GCAGCCCTGC
GGCTGTGTGA AGTCTGGCC CAAGCAGCTC AACGAGGACT GCAGAAAAC GCAGCCCTGC
GACCACACCA AGGGCTGGGA ATGCAACTTC GCGGCAGCT CCACGCTCT GAAGGGATC
TGCAGAGCTC AGTCAGAGG CAGACCTGT GAATATACT CCAGAATCTA CCAAAACGG
GAAAGTTTC AGCCCAACTG TAAACATCAG TGCCATGTGA TTGGATGGG CCGGGGGCT
TGCAATCTC TGTGTCCCA AGAACTATCT CTCCCACT TGGCTGTCC CAACCTCGG
CTGTCAAG TTACCGGCA GTCTGCGAG GAGTGGTCT GGAAGGGA TAGTATCAAG
GACCCATGG AGGACAGGA CGGCTCTCT GCGAAGGGC TGGGATGGA TGCTCCGAG
GTGGAGTGA CGAGAAACAA TGAATTGATT GCAGTTGGA AAGGAGCTC ACTGAAGCG
CTCCCTGTT TTGGAATGA GCTCGCATC CTATACAAC CTTTACAAG CCAGAAATGT
ATTGTTCAA CAACATCATG GTCCAGTGC TCAAAGACT GGGAACTGG TATCTCCACA
CGAGTTACA ATGACAAOC TGAGTCCCG GTACAGCAGC CTGTGAAAG AACCCGGAT TTGTGAGGTG
CGGCTGTIG GACAGCCAGT GATGTTACT CAGGTTTACT TACGCTGGAT GTTTGAGTGT CAGCAAGAAC
AAGAAATCC CCGAACCAT ACTGGGTTC CTGGTGGAC GGCGATGCT GCAGCCCCA GCTGACCCAG
CGGCCCAAGT ACTGGGTTC CTGGTGGAC GGCGATGCT GCAGCCCCA GCTGACCCAG
ACTGTGAAGA TGGGTTCCT CTGGAGATG GGGGAGACAT TTTCAGAA CGTCATGATG
ATCCAGTCT CCAATGCAA CTACAATGC CTACAATGC ATGAAGCAG GTTTCCTTC



Human Genome Sciences, Inc.
Sequence Worksheet
HLFBE49XX:

TACAGGCTGT TCCAATGACA TTACACAAATT TAGGGACTAA ATGCTACCTG GGTTCACAGG
GCACACCTAG ACCAAACAAG GCAGAAAGAGT GTACAGATCA GAATCATGGA GAAATGGGC
GGGGGIGGIG TGGGTGATGG GACTCATTTGT AGAAAGGAAG CCTTCCTCAT TCTTGAGGAG
CATTAAAGGTA TTTCGAAACT CCAAGGGIG CTGGTGGGA TGGACACTAA TGCAGCCACG
ATTGGAGAAT ACTTTCCTC ATAGTATGG ACCACATGTT ACTGCTTCAT TTTGGAGCTT
GTGGAGTGA TGACTTCTG TTTTCTGTTT GTAAATTATT TGCTAAGCAT ATTTCCTCA
GGCTTTTTC CTMTGGGT TCTACAGTGG TAAAAGAGAT AATAAGATTA GTTGACACAGT
TTAAAGCTTT TATTGTCCT TTGACAAAAG TAAATGGAG GCATTCOCAT CCTTCCTGG
AGGGGACAC TCCATGAGT TCTGIGAGAG GCAGCTATCT GCACCTTAA CIGCAACACAG
AAATCAGGIG TTTTAAAGACT GAATGTTTTA TTTATCAAAA TGTAGCTTTT GGGAGGGAG
GGGAAATGTA ATACTGGAAT AATTGTAAG TGAATTTAAT TTTATATTTCA GTCAAAAGAT
TTTATTTTATG GAATTAACCA TTTAATAAAG AAATATTTAC CTAAAAAAA AAAAAAAA
AAA*

Sequence Notes

Purchase Order # 70038

BILL AND SHIP TO ABOVE ADDRESS

Vendor Ref. #

Requisitioner to complete in clear, legible text

Date request filled out: 5/15/00

Requisitioner: Donna Dimick

Ext.: 2147

Building: 9430 Floor: 18F Lab: 6 DISC.

Suggested vendor: ATC

Use this vendor only: ☒ Yes

Date needed: 5/24/00

					USER:	PURCHASE ORDER		STATUS
PART #	QTY	*U/M	DESCRIPTION	PAGE	UNIT \$	TOTAL \$	INVOICE	
	1		1 vial ATCC deposit # 75804		Free	\$0.00	<input checked="" type="checkbox"/>	
	1		vial ATCC deposit		Free	\$0.00	<input checked="" type="checkbox"/>	
	1		vial ATCC deposit		Free	\$0.00	<input checked="" type="checkbox"/>	
					TOTAL	\$0.00	TOTAL	<input checked="" type="checkbox"/>

ACCT. CODES			EXTRA CHARGES	SIGNATURES
LINE #	DEPT. #:	ACCT. #:	Shipping & Handling: \$29.50	Requisitioner/Date: <i>Donna M. Mable</i>
	165	6010	Disc. Fee:	Approved by/Date:
			Freight:	Approved by/Date:
	PROJECT ACCT. #:		Misc:	Approved by/Date:
	TAXABLE? <input type="checkbox"/> YES <input type="checkbox"/> NO			

* Suggest examples - cs, ea, units, pk, g, ml., IL

WHITE COPY – Purchasing

YELLOW COPY - Administration

PINK COPY – Requisitioner's Confirmation

GOLD COPY – Requisitioner's Original

rev. 8/99

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10801 University Boulevard
Manassas, Virginia, 20110-2209 USA
703-365-2700 FAX: 703-365-2750
EMAIL: sales@atcc.org

PACKING LIST

06/12/2000

ATCC 10801 University Blvd. Manassas, VA 20110-2209 USA
EMERGENCY RESPONSE: Chemtrec (800) 424-9300 or (202) 483-7616

SHIP-TO:

SALES ORDER # SO171485

10014301
Human Genome Sciences Inc
9410 Key West Ave
Rockville, MD 20850
USA

BILL-TO:

29219
Human Genome Sciences Inc
Accounts Payable
9410 Key West Ave
Rockville, MD 20850

ATTN:

TEL #: 301-309-8504 FAX#: 301-309-8512

ATTN: Dimke, Donna

TEL #: 301-610-5790 FAX#: 301-279-0175

CUSTOMER P.O. #: 70038

SOLD TO: 29219
ORDER DATE: 06/05/00
SALESPERSON: nhiggins
FOB: Manassas, VA
BOL:
SHIPPED VIA: Alert
SHIP DATE: 06/12/00
FREIGHT LIST
FZ-NON

#	B S L	ITEM NUMBER	U M	QTY SHIP	QTY B.O.	DESCRIPTION	PRICE	NET PRICE
001	1	75804 HEAT	EA	1	0	RESTRICTED PATENT, REFER <u>HLFBE49XY</u> ALL ORDERS	0.00	0.00
002	1		EA	1	0	RESTRICTED PATENT, REFER ALL ORDERS	0.00	0.00
003	1		EA	1	0	RESTRICTED PATENT, REFER ALL ORDERS	0.00	0.00

Taxable Total: 0.00
Tax[1]: 05.00% Tax[2]: 00.00% Tax[3]: 00.00%
Amount Pre-Paid: 0.00

Line Total: 0.00
Total Tax: 0.00

Shipping & Handling: 24.50

? Discount: 0.00
USD Grand Total: 24.50

Page # 001

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FIG. 1A

ATGAGCTCCCGAATCGTCAGGAGGAGCTCGCCTTAGTCGTCAACCCTTCTCCACTTGACCAGG
M S S R I V R E L A L V V T L L H L T R

GTGGGCTCTCCACCTGCCCCGCTGACTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG
V G L S T C P A D C H C P L E A P K C A

CCGGAGTCGGGCTGTGTCGGGACGGCTGCGGCTGTGTAAGGTCTGCGCCAAGCAGCTC
P G V G L V R D G C G C C K V C A K Q L

AACGAGGACTGCAGAAACGAGCCCTGCGACCACCAAGGGGCTGGAATGCACTTC
N E D C R K T Q P C D H T K G L E C N F

GGCGCCAGCTCCACCGCTCTGAAGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCCTGT
G A S S T A L K G I C R A Q S E G R P C

GAATATACTCCAGAATCTACCAAAACGGGGAAGTTTCCAGCCCACTGTAAACATCAG
E Y N S R I Y Q N G E S F Q P N C K H Q

TGCACATGTATTGGATGGCGCGGGGCTTGCAATTCCTCTGTGTCCCAAGACTATCT
C T C I G W R R G A C I P L C P Q E L S
CTCCCAACTTGGGCTGTCCCAACCCTCGGCTGTCAAGTTACCGGGCAGTGCTGCGAG
L P N L G C P N P R L V K V T G Q C C E
MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

FIG. 1B

GAGTGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGCGCCTCCTT
E W V C D E D S I K D P M E D Q D G L L

GGCAAGGGGCTGGGATTTCGATGCCCTCCGAGGTGGAGTTGACGAGAACAATGAATTGATT
G K G L G F D A S E V E L T R N N E L I

GCAGTTGGAAGAAGGCAGCTCACTGAAGCGGCTCCCTGTTTGTGGAATGGAGCCTCGCATC
A V G K G S S L K R L P V F G M E P R I

CTATACAACCCCTTTACAAGGCCAGAAATGTATTGTTCAACAACACTTCATGCTCCAGTGC
L Y N P L Q G Q K C I V Q T T S W S Q C

TCAAAGACCTGTGGAAGTGTATCTCCACACGAGTTACCAATGACAACCCCTGAGTGCCGC
S K T C G T G I S T R V T N D N P E C R

CTTGTGAAGAACCCTGGATTGTTGTGAGGTGCGGCTTGTGGACAGCCAGTGTTACAGCAGC
L V K E T R I C E V R P C G Q P V Y S S

CTGAAAAAGGGCAAGAATGCAGCAAGACCAAGAATCCCCGAAACCAGTCAGGTTTACT
L K K G K K C S K T K K S P E P V R F T

MATCH WITH FIG. 1C

MATCH WITH FIG. 1B

FIG. 1C

TACGCTGGATGTTTGAGTGTGAAGAATAACCGGCCCAAGTACTGCGGTTCCCTGCGTGAC
Y A G C L S V K K Y R P K Y C G S C V D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCCGTTCCCTGCCGAGAT
G R C C T P Q L T R T V K M R F P C E D

GGGAGACATTTTCCAGAAGCGTCATGATGATCCAGTCCCTCCAATGCACTACAACCTGC
G E T F S K N V M M I Q S S K C N Y N C

CCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTCCAATGA
P H A N E A A F P F Y R L F Q *

FIG. 2A

1 MSSRIVRELALVTLHLTRVGLSTCPADCHCPLCAPGVGLVRDGC 50
|||.
1 MSSSTFRTLAVAVTLHLTRLALSTCPAACHCPLCAPGVGLVRDGC 50

51 GCCCKVC AKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC 100
|||||
51 GCCCKVC AKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC 100

101 EYNSRIYQNGESFQPNCKHQCTCIGWRGACIPLCPQELSLPNLGCPNPR 150
MATCH WITH FIG. 2B

305

325800-317

MATCH WITH FIG. 2A

FIG. 2B

101 EYNSRIYQNGESFQPNCKHQCTCID.GAVGCIPLCPQELSLPNLGCPNPR 149
151 LVKVTCQCCCEEWVCDEDSIKDPMEDQDGLGKGLGFDASEVELTRNNELI 200
150 LVKVSQCCCEEWVCDEDSIKDSLDDQDDL...LGLDASEVELTRNNELI 195
201 AVGKGSSLKRLPVFGMEPRILYNPL..QGQKCIVQTTWSQCSKTCGTGI 248
196 AIGKGSSLKRLPVFGTEPRVLFNPLHAHQKCIVQTTWSQCSKSCGTGI 245
249 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKCSKTKKSPPEVR 298
246 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKCSKTKKSPPEVR 295
299 FTYAGCLSVKKYRPKYCGSCVDGRCCCTPQLTRTVKMRFPCEDETFSKNV 348
296 FTYAGCSSVKKYRPKYCGSCVDGRCCCTPLQTRTVKMRFRCEDEGMFSKNV 345
349 MMIQSSKCNYNCPHANEAFPFYRLFQ 375
346 MMIQSCKCNYNCPHPNEASFRLYSLFN 372

5 of 5

325800-317

HLFBE49
Sequencher™ "CORRECTED CTGF-2 PROJECT"

HLFBEXXF1A
HLFBEXXRA
HLFBEXXR
HLFBE49XX

#1

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GGCACGAGCCCGCCGCGCCAGCCCTCGCCTCCCTGCCCACCGGGCCACCGCGCCGCC
GGCACGAGCCCGCCGCGCCAGCCCTCGCCTCCCTGCCCACCGGGCCACCGCGCCGCC
GGCACGAGCCCGCCGCG:GCC:AGCCCTCGCCTCCCTGCCCACCGG:CCCACCGCGCCGC:

HLFBEXXF1A
HLFBEXXRA
HLFBEXXR
HLFBE49XX

#62

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ACCCCGACCCCGCTGCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTGCG
ACCCCGACCCCGCTGCG:ACGGGCTGTCCGCTGCACACCAGCTTGTTGGTGTCTTCGTGCG

HLFBEXXF1A
HLFBEXXRA
HLFBEXXR
HLFBE49XX
HLFBEXXR1

#123

ACCCCGACCCCGCTGCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTGCG
CGCGCTCGCCCCGGGCTACTCCTGCGCGCCNCAATGAGCT
CGCGCTCGCCCCGGGCTACTCCTGCGCGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG
CGCGCTCGCCCCGGGCTACTCCTGCGCGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG
CGCGCTCGCCCCGGGTTACTCCTGCGCGACACAATGAGCTCCCGAATCGTCAGGGAGCTCG
CGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG

HLFBEXXRA
HLFBEXXR
HLFBE49XX
HLFBEXXR1

#184

CGCGCTCGCCCCGGGCTACTCCTGCGCGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG
CCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCTCCACCTGCCCCGCTGCCTG
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CCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCTCCACCTGCCCCGCTGCCTG

HLFBEXXRA
HLFBEXXR
HLFBE49XX
HLFBEXXR1

#245

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CCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACGGCTGC
CCACTGCCCCC
CCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACGGCTGC

HLFBEXXRA
HLFBEXXR
HLFBE49XX
HLFBE49R
HLFBEXXR2A

#306

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GCAAAACGCAGCCCTGCG
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HLFBE49
Sequencher™ "CORRECTED CTGF-2 PROJECT"

HLFBEXXRA
HLFBEXXR
HLFBE49XX
HLFBE49R
HLFBEXXR2A
HLFBEXXR2

#367

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GCCAGCTCCACCGCTCTGAAGGGGATCTG

HLFBEXXRA
HLFBEXXR
HLFBE49XX
HLFBE49R
HLFBEXXR2A
HLFBEXXR2

#428

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CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAACGGGGAA

CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAACGGGGAA

HLFBEXXRA
HLFBEXXR
HLFBE49XX
HLFBE49R
HLFBEXXR2A
HLFBEXXR2
HLFBEXXR2BA
HLFBEXXR2B

#489

AG
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AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGGATGGCGCCGGGGGGCTTGCA
AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
CATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
TCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA

HLFBE49XX
HLFBE49R
HLFBEXXR2A
HLFBEXXR2
HLFBEXXR2BA
HLFBEXXR2B

#550

AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA

TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT

TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT

HLFBE49XX
HLFBE49R
HLFBEXXR2A
HLFBEXXR2
HLFBEXXR2BA
HLFBEXXR2B
HLFBEXXR3

#611

CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
CAAAG
CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
GAGGATAGTATCAAGGACCCC

CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC

HLFBE49
Sequencher™ "CORRECTED CTGF-2 PROJECT"

HLFBE49XX	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGGGCTGGGATTTCGATGCCTCCGAGGTGGAGT
HLFBEXXR2A	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTTCGATGCCTCCGAGGTGGAGT
HLFBEXXR2	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTTCGATGCCTCCGAGGTGGAGT
HLFBEXXR2BA	ATGGAGGACCAGGACGGCCTCCTTG
HLFBEXXR2B	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTTCGATGCCTCCGAGGTGGAGT
HLFBEXXR3	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTTCGATGCCTCCGAGGTGGAGT
HLFBEXXR3BA	GATGCC TCCGAGGTGGAGT
HLFBEXXR3B	TGCC TCCGAGGTGGAGT

#672

ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTTCGATGCCTCCGAGGTGGAGT

HLFBE49XX	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR2A	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR2	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR2B	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR3	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR3BA	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR3B	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT

#733

TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT

HLFBE49XX	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR2A	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR2	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR2B	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR3	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR3BA	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR3B	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA

#794

TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA

HLFBE49XX	ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA
HLFBEXXR2A	ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA
HLFBEXXR2	ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA
HLFBEXXR2B	ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA
HLFBEXXR3	ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA
HLFBEXXR3BA	ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA
HLFBEXXR3B	ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA
HLFBEXXR4A	GTATCTCCACACGAGTTACCA
HLFBEXXR4	ATCTCCACACGAGTTACCA

#855

ACAACCTTCATGGTCCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCA

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HLFBE49XX ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR2A ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCC
HLFBEXXR2 ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR2B ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR3 ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR3BA ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR3B AT
HLFBEXXR4A ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR4 ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR4B GCC TTGTG AAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG

#916

ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG

HLFBE49XX ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR2 ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR2B ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR3 ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR3BA ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR4A ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR4 ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR4B ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC

#977

ACAGCCAGTGACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC

HLFBE49XX GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR2 GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR2B GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR3 GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR3BA GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR4A GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR4 GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR4B GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT

#1038

GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT

HLFBE49XX GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR2 GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR2B GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCC
HLFBEXXR3 GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR3BA GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR4A GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR4 GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR4B GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR5 CC GATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR5A TGC TGCACGC CCCAGCTGACCAGGACTGTGAAGATGCG

#1099

GCGGTTCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG

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HLFBE49XX	GTTCCCCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAA
HLFBEXXR2	GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCT
HLFBEXXR3	GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA
HLFBEXXR3BA	GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA
HLFBEXXR4A	GTTCCGCTGCGAAGA
HLFBEXXR4	GTTCCGCTGCGAAGA
HLFBEXXR4B	GTTCCGCTGCGAAGATGG
HLFBEXXR5	GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA
HLFBEXXR5A	GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA

#1160

HLFBE49XX	TGCAACTACAAC TGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCCAAT
HLFBEXXR3	TGCAACTACAAC TGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTT : AAT
HLFBEXXR3BA	TGCAACTACAAC TGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTT : AAT
HLFBEXXR5	TGCAACTACAAC TGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTT : AAT
HLFBEXXR5A	TGCAACTACAAC TGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTT : AAT
HLFBEXXF	TCCCTTCTACAGGCTGTTT : AAT

#1221

HLFBE49XX	GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGACCAAAC
HLFBEXXR3	GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC : AAAC
HLFBEXXR3BA	GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC : AAAC
HLFBEXXR5	GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC : AAAC
HLFBEXXR5A	GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC : AAAC
HLFBEXXF	GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC : AAAC

#1282

HLFBE49XX	AAGGGAGAAGAGTGTGAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT
HLFBEXXR3	AAGGGAGAAGAGTGTGAGAATCAGAATCATGGAGAAAATGG
HLFBEXXR3BA	AAGGGAGAAGAG
HLFBEXXR5	AAGGGAGAAGAGTGTGAGAATCAGAATCATGGAGAAAATGGGCGGNGGTGGTGTGGGTGAT
HLFBEXXR5A	AAGGGAGAAGAGTGTGAGAATCAGAATCATGGAGAAAATGGGCGGNGGTGGTGTGGGTGAT
HLFBEXXF	AAGGGAGAAGAGTGTGAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT
HLFBEXXR6BA	GGGAN NAGAGT GTCAGAATCAGAATCNTGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT
HLFBEXXR6B	GTCAGAATNAGAAATCATGGANAAAATGGGCGGNGGTGGTGTGGGTGAT
HLFBEXXR6	AAAATGGNCGGNGGTGGTGTGGGTGAT

#1343

AAGGGAGAAGAGTGTGAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT

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HLFBE49XX
HLFBEXXR5
HLFBEXXR5A
HLFBEXXF
HLFBEXXR6BA
HLFBEXXR6B
HLFBEXXR6
HLFBEXXR6A
HLFBEXXFA
#1404

GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGGTATTTGAAAC
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GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGGTATTTGAAAC
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AGGTATTTGAAAC

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HLFBEXXR6B
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HLFBEXXFA
#1465

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+ + + + ++ ++
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TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC

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HLFBEXXF
HLFBEXXR6BA
HLFBEXXR6B
HLFBEXXR6
HLFBEXXFA
HLFBEXXR7A
#1526

TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
+
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TGT

HLFBE49XX
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HLFBEXXR5A
HLFBEXXF
HLFBEXXR6BA
HLFBEXXR6B
HLFBEXXR6
HLFBEXXFA
HLFBEXXR7A
#1587

ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTTGGAGTTGATGACTTTCTGT
+ +
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TNTCTGTTTGTAATAATTATTTGCTAAGCATATTTTCTCTAGGCTNTTTTTTCCTTTTGGGGTTC
TTTCTGTTTGTAATAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
+ + + + + +

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HLFBE49XX
HLFBEXXR5
HLFBEXXR5A
HLFBEXXF
HLFBEXXR6BA
HLFBEXXR6B
HLFBEXXFA
HLFBEXXR7A
#1648

TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
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TACAGTNGTAAAAGAGATAATAAGATTAGTTGNACAGTTNAAAGCTTTTATTCGTCCTTTG
TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG

HLFBE49XX
HLFBEXXR5
HLFBEXXR5A
HLFBEXXF
HLFBEXXR6BA
HLFBEXXR6B
HLFBEXXFA
HLFBEXXR7A
#1709

TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
+ + + +
ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGGAGGGGGACACTCCATGAGTGTCTG
ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
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ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG

HLFBE49XX
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HLFBEXXF
HLFBEXXR6BA
HLFBEXXR6B
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HLFBEXXR7A
HLFBEXXR8
HLFBEXXR8A
#1770

ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
+ +
TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
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TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCANGTGTTTTAAGACTGAATG
TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
TGAGAGGCAGCTATCTGCACTCTAAACTGCANNCAGAAATCAGGTGTTTTAAGACTGAANG
TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
CTGNAAACAGANATCAGGTGTTTTAAGACTGAATG
AAACAGAAATCAGGTGTTTTAAGACTGAATG

HLFBE49XX
HLFBEXXR5
HLFBEXXR5A
HLFBEXXF
HLFBEXXR6BA
HLFBEXXR6B
HLFBEXXFA
HLFBEXXR7A
HLFBEXXR8
HLFBEXXR8A
#1831

TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
+ ++ + +
TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
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TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
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HLFBE49XX
HLFBEXXR5
HLFBEXXR5A
HLFBEXXF
HLFBEXXR6BA
HLFBEXXFA
HLFBEXXR7A
HLFBEXXR8
HLFBEXXR8A
#1892

TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
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TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
TAAATGATTTTAATTTTATATTCAGNGAAAAGATTTTA
TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

HLFBE49XX
HLFBEXXF
HLFBEXXR6BA
HLFBEXXFA
HLFBEXXR8
HLFBEXXR8A
#1953

TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
+ +
AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAA
AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAA
AAGAAATATTTACCT AA
AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAA
AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAA
AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAA
AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAA
AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAA

1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
1 M S S R I A R A L A L V V T L L H L T R 20

61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGC GCG 120
21 L A L S T C P A A C H C P L E A P K C A 40

121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
41 P G V G L V R D G C G C C K V C A K Q L 60

181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
61 N E D C S K T Q P C D H T K G L E C N F 80

241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
81 G A S S T A L K G I C R A Q S E G R P C 100

301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
101 E Y N S R I Y Q N G E S F Q P N C K H Q 120

361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCAAGAACTATCTCTC 420
121 C T C I D G A V G C I P L C P Q E L S L 140

421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
141 P N L G C P N P R L V K V T G Q C C E E 160

FIG. 1A

481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
161 W V C D E D S I K D P M E D Q D G L L G 180

541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
181 K E L G F D A S E V E L T R N N E L I A 200

601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGAATGGAGCCTCGCATCCTA 660
201 V G K G S S L K R L P V F G M E P R I L 220

661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACCTTCATGGTCCCAGTGCTCA 720
221 Y N P L Q G Q K C I V Q T T S W S Q C S 240

721 AAGACCTGTGGAACCTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
241 K T C G T G I S T R V T N D N P E C R L 260

781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
261 V K E T R I C E V R P C G Q P V Y S S L 280

841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTTACTTAC 900
281 K K G K K C S K T K K S P E P V R F T Y 300

901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCTGCGTGGACGGC 960
301 A G C L S V K K Y R P K Y C G S C V D G 320

FIG. 1B

961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTCCGCTGCGAAGATGGG 1020
321 R C C T P Q L T R T V K M R F R C E D G 340

1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAAC TGCCCG 1080
341 E T F S K N V M M I Q S C K C N Y N C P 360

1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
361 H A N E A A F P F Y R L F N D I H K F R 380

1141 GACTAA 1146
381 D * 382

FIG. 1C

FIG. 1A

ATGAGCTCCCG^{C.}ATCG^CAGGG^CAGCTCGCCTTAGTCGTACCCCTTCTCCACTTGACCAGG
M S S R I ~~A~~ R ~~A~~ L A L V V T L L H L T R

~~CTGGG~~CTCTCCACCTGCCCGCTG^CCTGCCACTGCCCCCTGGAGGGCCCAAGTGGCG
~~L~~ ~~A~~ L S T C P A ~~A~~ C H C P L E A P K C A

CCGGAGTCGGGCTGGTCCGGGACGGCTGGGGCTGTGTAAGTCTGCCCAAGCAGCTC
P G V G L V R D G C G C C K V C A K Q L

AACGAGGACTGCAG^CAAAAACGCAGCCCTGCCGACCACCAAGGGCTGGAATGCAACTTC
N E D C ~~K~~ K T Q P C D H T K G L E C N F

GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAAGGGCAGACCCCTGT
G A S S T A L K G I C R A Q S E G R P C

GAATATACTCCAGAATCTACCAAAACGGGGAAGTTTCCAGCCCAACTGTAAACATCAG
E Y N S R I Y Q N G E S F Q P N C K H Q

TGCACATGTATTG^TATGGCGCGCGGG^TCTGCATTCCTCTGTGTCCCAAGAACTATCT
C T C I ~~A~~ ~~G~~ ~~R~~ ~~A~~ ~~V~~ ~~G~~ C I P L C P Q E L S

CTCCCAACTTGGGCTGTCCCAACCCCTCGGCTGTCAAGTTACCGGGCAGTGCTGGCAG
L P N L G C P N P R L V K V T G Q C C E
MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

FIG. 1B

GAGTGGGCTCTGTGACGAGGATAGTATCAAGGACCCCATGAGGAGCAGCGCCCTCCTT
E W V C D E D S I K D P M E D Q D G L L

GGCAAGG^AGGCTGGGATTCGATGCCCTCCGAGGTGGAGTTGACGAGAACAATGAATTGATT
G K ~~E~~ L G F D A S E V E L T R N N E L I

GCAGTTGGAAAAGGCGAGCTCACTGAAGCGGCTCCCTGTTTGGGAATGGAGCCTCGCATC
A V G K G S S L K R L P V F G M E P R I

CTATACAACCCCTTTACACAAGGCCAGAAATGTATTGTTCAACAACCTTCATGGTCCCAAGTGC
L Y N P L Q G Q K C I V Q T T S W S Q C

TCAAGACCTGTGGAAGTGTATCTCCACACGAGTTACCAATGACAACCCCTGAGTGCCGC
S K T C G T G I S T R V T N D N P E C R

CTTGTGAAGAACC CGATTGTGAGGTGCGGCTTGTGGACAGCCAGTGTACAGCAGC
L V K E T R I C E V R P C G Q P V Y S S

CTGAAAAAGGCGACAAGAAATGCAGCAGACCAAGAATCCCCGAACCACTCAGGTTTACT
L K K G K K C S K T K K S P E P V R F T

MATCH WITH FIG. 1C

ATGAGCTCCGATCG^CAGGG^CAGCTCGCCTTAGTCGTACCCCTTCTCCACTTGACCAGG
M S S R I ~~A~~ R ~~A~~ L A L V T L L H L T R

^CGTGGGCTCTCCACCTGCCCGCTG^CACTGCCACTGCCCTGGAGG^CCCCCAAGTGGCGG
~~A~~ L S T C P A ~~A~~ C H C P L E A P K C A

CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTG^CTGTAAAGTCTGCGGCAAGCAGCTC
P G V G L V R D G C G C C K V C A K Q L

AACGAGGACTGCAG^CAAAAACGAGCCCTGCGACACACCAAGGGCTGGAATGCAACTTC
N E D C ~~A~~ K T Q P C D H T K G L E C N F

GGCGCCAGCTCCACGCTCTGAAGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT
G A S S T A L K G I C R A Q S E G R P C

GAATATAACTCCAGAATCTACCAAAACGGGAAAGTTTCCAGCCCAACTGTAAACATCAG
E Y N S R I Y Q N G E S F Q P N C K H Q

TGCACATGTATTG^TATGGCGCCGG^CCTGCAATTCCTCTGTGTCCTCCCAAGAACTATCT
C T C I ~~A~~ ~~R~~ ~~A~~ ~~A~~ C I P L C P Q E L S

CTCCCCAACTTGGGCTGTCCCAACCTCGGCTGGTCAAAGTTACCGGGCAGTGTGGAG
L P N L G C P N P R L V K V T G Q C C E
MATCH WITH FIG.1B

FIG.1A

MATCH WITH FIG.1A

GAGTGGGTCGTGACGAGGATAGTATCAAGGACCCCATGGAGGACGAGGCGCCTCCTT
E W V C D E D S I K D P M E D Q D G L L

^AGGCAAGGCTGGGATTCGATGCCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G K ~~G~~ L G F D A S E V E L T R N N E L I

GCAGTTGGAAAGGAGCTCACTGAAGCGGCTCCCTGTTTTTGGAAATGGAGCCTCGCATC
A V G K G S S L K R L P V F G M E P R I

CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAACAACCTTCATGGTCCCAGTGC
L Y N P L Q G Q K K C I V Q T T S W S Q C

TCAAAGACCTGTGGAACCTGGTATCTCCACAGAGTTACCAATGACAACCTGAGTGCCGC
S K T C G T G I S T R V T N D N P E C R

CTTGTGAAAGAACCCGGATT^{*T.G}STGAGGTGGGCCCTTGTGGACAGCCAGGTGTACAGCAGC
L V K E T R I C E V R P C G Q P V Y S S

CTGAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAAGTCAGGTTTACT
L K K G K K C S K T K K S P E P V R F T
MATCH WITH FIG.1C

FIG.1B

MATCH WITH FIG.1B

TACGCTGGATGTTGAGTGAAGAAATACGGCCCAAGTACTGCGGTTCTCCTGCGTGAC
Y A G C L S V K K Y R P K Y C G S C V D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCC^GCTGCGAAGAT
G R C C T P Q L T R T V K M R F ^P C E D ^R

GGGAGACATTTTCCAAGAAGCTCATGATGATCCAGTCT^GCAAAATGCAACTACAAC TGC
G E T F S K N V M M I Q S ^S K C N Y N C ^C

CCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTC^GAAATGACATTCAACA
P H A N E A A F P F Y R L F ^N D I H K

TTTAGG GAC TAA
F R D *

FIG.1C

~~1 MSSRIHVRELALVWTLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGC 50~~
~~||||...|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||~~
~~1 MSSSTFRTLAVAVTLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGC 50~~

51 GCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC 100

~~|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||~~
51 GCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC 100

101 EYNSRIYNGESFQPNCKHQCTCIGWRRGACIPLCPQELSPLNLGCPNPR 150

~~MATCH WITH FIG.2B~~

FIG.2A

FIG. 1A

ATGAGCTCCCGAATCGTCAGGAGGAGCTCGCCTTAGTCGTCAACCCTTCTCCACTTGACCAGG
M S S R I V R E L A L V V T L L H L T R

GTGGGCTCTCCACCTGCCCCGCTGACTGCCACTGCCCCCTGGAGGGCCCAAGTGCCG
V G L S T C P A D C H C P L E A P K C A

CCGGAGTCGGGCTGCTCCGGGACGGCTGCGGCTGTGTAAAGTCTGCCCAAGCAGCTC
P G V G L V R D G C G C C K V C A K Q L

AACGAGACTGCAGAAACGCGACCCCTGCCGACCACCAAGGGGCTGGAATGCCACTTC
N E D C R K T Q P C D H T K G L E C N F

GGCGCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCCTGT
G A S S T A L K G I C R A Q S E G R P C

GAAATATACTCCAGAATCTACCAAAACGGGGAAGTTTCCAGCCCAACTGTAAACATCAG
E Y N S R I Y Q N G E S F Q P N C K H Q

TGCACATGTATTGGATGGCGCGGGGGCTTGCAATTCCTCTGTGTCCCAAGAACTATCT
C T C I G W R R G A C I P L C P Q E L S

CTCCCCAACTTGGGCTGTCCCAACCCCTCGGCTGTCAAAAGTTACCGGGCAGTGCTGCCGAG
L P N L G C P N P R L V K V T G Q C C E
MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

FIG. 1B

GAGTGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGCGCCTCCTT
E W V C D E D S I K D P M E D Q D G L L

GGCAAGGGGCTGGGATTCCGATGCCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G K G L G F D A S E V E L T R N N E L I

GCAGTTGGAAGAAGGCAGCTCACTGAAGCGGCTCCCTGTTTGGGAATGGAGCCTCGCATC
A V G K G S S L K R L P V F G M E P R I

CTATACAACCCCTTTACAAGGCCAGAAATGTATTGTTCAACAACCTTCATGGTCCAGTGC
L Y N P L Q G Q K C I V Q T T S W S Q C

TCAAAGACCTGTGGAACCTGGTATCTCCACACGAGTTACCAATGACAACCCCTGAGTGCCGC
S K T C G T G I S T R V T N D N P E C R

CTTGTGAAGAACCCTGGATTGTGTGAGGTGCGCCTTGTGACAGCCAGTGTACAGCAGC
L V K E T R I C E V R P C G Q P V Y S S

CTGAATAAGGGCAAGAATGCAGCAAGACCAAGAAATCCCCGAACCACTCAGGTTACT
L K K G K K C S K T K K S P E P V R F T

MATCH WITH FIG. 1C

MATCH WITH FIG. 2A.

FIG. 2B

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|||||:..:|||||
101 EYNSRIYONGESFQPNCKHQCTCID.GAVGCIPLCPELSPNLGCPNPR 149

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151 LKVTGQCCCEWVCDEDSIKDPMEDQDGLGKGLGFDA SEVELTRNNELI    200
      |||||.||||||.||||||.:.:|||||:|   ||:|||||.||||||
150 LVKVSQCCEEWVCDEDSIKDSLDDQDDL...LG LDASEVELTRNNELI    195

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201  AVGGSSLKRLPVFGMEPRILYNPL..QGQKCIVQTTSWSQCSKTCTGTGI  248
      |:||||| | | | | | | | | | | | | | | | | | | | | | | |
196  AIGKSSLKRLPVFGTEPRVLEPNPLHAHQKCIVQTTSWSQCSKSCGTGI  245

```

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249 STRVTNDNPECR LVKETRICEV R P C G Q P V Y S S L K K G K K S K T K K S P E P V R 298
      |||||
246 STRVTNDNPECR LVKETRICEV R P C G Q P V Y S S L K K G K K S K T K K S P E P V R 295

```

```

299 FTYAGCLSVKKYRPKYCGSCVDGRCTPQLTRTVKMRFPCEDETF SKNV 348
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
296 FTYAGCSSVKKYRPKYCGSCVDGRCTPQLTRTVKMRFRCEDEGEMF SKNV 345

```

349 M M I Q S K C N Y N C P H A N E A F P F Y R L F Q 375
 ||||| : ||||| ||||| : |||. | . : | . | .
 346 M M I Q S K C N Y N C P H P N E A S F R L Y S L F N 372

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1 MSSRIVRELALVTLHL.TRVGLS.TCPADCHCPLE.APKCARGVLVR 47
  | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
1 MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAPHCPAGVSLVL 50

48 DGGCCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEG 97
  ||||| : ||||| . | . : ||||| ||||| : || . . . . . | : | . : |
51 DGGCCRCVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK.DG 99

98 RPCEYNSRIYQNGESEFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCPR 147
  || : . . . . : | . . . . . | . . . . . | . . . . . | . . . . . |
100 APCVFGGSVYRSGESFQSSCKYQCTCLD.GAVGCVPLCSMDVRLPSPDCP 148
148 NPRLVKVTGQCCCEEWCDEDSIKDPMEDQDGLGKGLGFDASEVELTRNN 197
  || || : . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
149 FPRRVKLPKCKCKEWCDEPKDRTAV. . . . . GPALAAVRL EDT . . . 186
198 ELIAVGKGSSLKRLPVEGMEPRILYNPLQGGQKCIVQTTSWSQCSKTCGTG 247
187 . . . . . FGPDP T M . . . . . RANCLVQTT EWSACS KTCGMG 215

248 ISTRVTNDNPECRLVKETRICEVRPCGQPVYSSSLKKGKCSKTKKSPEPV 297
  ||||| ||||| . ||||| : : ||||| : : ||||| : : ||||| : : |||||
216 ISTRVTNDNTFCRL EKQSRLCMV RPCEADLEENIKKGKCI RTPKIAKPV 265
298 RFTYAGCLSVKKYRPKYCGSCVDGRCC T PQLTRTVKMRFPCEDEGETFSKN 347
  : | . . . . | | | | . : : | | | | . : : | | | | . : : | | | |
266 KFELSGCTSVKTYRAKFCGVCTDGRCC T PHRTTTL PVEFEKCPDGEIMKN 315

348 VMMIQSSKCNYNCPHANE. . AAFPYRL FQ 375
  : | : | . . . : | : | | | | . | : . . . . : : : : .

316 MMFIKTCACHYNC PGDNDIFESLYRKMYG 345

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